

0967361 08-001

GGACTAATCTGTGGGAGCAGTTTATTCCAGTATCACCCAGGGTGCAGCCACACCAGGACTGT
GTTGAAGGGTGTTTTTTTTTCTTTTAAATGTAATACCTCCTCATCTTTTCTTCTTACACAGTG
TCTGAGAACATTTACATTATAGATAAGTAGTACATGGTGGATAACTTCTACTTTTAGGAGGA
CTACTCTCTTCTGACAGTCTTAGACTGGTCTTCTACACTAAGACACCATGAAGGAGTATGTG
CTCCTATTATTCTCTGGCTTTGTGCTCTGCCAAACCCTTCTTTAGCCCTTCACACATCGCACT
GAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATGATGATG
ATGATGATGATGAGGACAACCTCTCTTTTTTCCAACAAGAGAGCCAAGAAGCCATTTTTTTTCCA
TTTGATCTGTTTCCAATGTGTCCATTTGGATGTCAGTGCTATTACGAGTTGTACATTGCTC
AGATTTAGGTTTGACCTCAGTCCCAACCAACATTCCATTTGATACTCGAATGCTTGATCTTC
AAAACAATAAAATTAAGGAAATCAAAGAAATGATTTTTAAAGGACTCACTTCACTTTATGGT
CTGATCCTGAACAACAACAAGCTAACGAAGATTACCCAAAAGCCTTTCTAACCACAAAGAA
GTTGCGAAGGCTGTATCTGTCCCACAATCAACTAAGTGAAATACCACTTAATCTTCCCAAT
CATTAGCAGAACTCAGAATTCATGAAAATAAAGTTAAGAAAATACAAAAGGACACATTCAA
GGAATGAATGCTTTACACGTTTTGGAAATGAGTGCAAACCCTCTTGATAATAATGGGATAGA
GCCAGGGGCATTTGAAGGGGTGACGGTGTTCCATATCAGAATTGCAGAAGCAAACTGACCT
CAGTTCCTAAAGGCTTACCACCAACTTTATTGGAGCTTCACTTAGATTATAATAAAATTTCA
ACAGTGGAACCTTGAGGATTTTAAACGATACAAAGAACTACAAAGGCTGGGCCTAGGAAACAA
CAAAATCACAGATATCGAAAATGGGAGTCTTGCTAACATACCACGTGTGAGAGAAATACATT
TGGAACAATAAACTAAAAAAATCCCTTCAGGATTACCAGAGTTGAAATACCTCCAGATA
ATCTTCCTTCATTCTAATTCAATTGCAAGAGTGGGAGTAAATGACTTCTGTCCAACAGTGCC
AAAGATGAAGAAATCTTTATACAGTGCAATAAGTTTATTCAACAACCCGGTGAAATACTGGG
AAATGCAACCTGCAACATTTTCGTTGTGTTTTGAGCAGAATGAGTGTTAGCTTGGGAACCTT
GGAATGTAATAATTAGTAATTGGTAATGTCCATTTAATATAAGATTCAAAAAATCCCTACATT
TGGAATACTTGAACCTCTATTAATAATGGTAGTATTATATATACAAGCAAATATCTATTCTCA
AGTGGTAAAGTCCACTGACTTATTTTATGACAAGAAATTTCAACGGAATTTTGCCAAACTATT
GATACATAAGGGGTTGAGAGAAACAAGCATCTATTGCAGTTTCCTTTTTTGCGTACAAATGAT
CTTACATAAATCTCATGCTTGACCATTCCTTTCTTCATAACAAAAAGTAAGATATTCGGTA
TTTAACACTTTGTATCAAGCACATTTTAAAAAGAACTGTACTGTAAATGGAATGCTTGACT
TAGCAAAATTTGTGCTCTTTTCAATTTGCTGTTAGAAAAACAGAATTAACAAAGACAGTAATGT
GAAGAGTGCATTACACTATTCTTATTCTTTAGTAACTTGGGTAGTACTGTAATATTTTTAAT
CATCTTAAAGTATGATTTGATATAATCTTATTGAAATTACCTTATCATGTCTTAGAGCCCGT
CTTTATGTTTTAAACTAATTTCTTAAATAAAGCCTTCAGTAAATGTTTATTACCAACTTGA
TAAATGCTACTCATAAGAGCTGGTTTGGGGCTATAGCATATGCTTTTTTTTTTTTTAATTATT
ACCTGATTTAAAAATCTCTGTAAAAACGTGTAGTGTTTCATAAAATCTGTAACTCGCATTTT
AATGATCCGCTATTATAAGCTTTTAAATAGCATGAAAATTGTTAGGCTATATAACATTGCCAC
TTCAACTCTAAGGAATATTTTTGAGATATCCCTTTGGAAGACCTTGCTTGGAAGAGCCTGGA
CACTAACAATTCTACACCAAATGTCTCTTCAAATACGTATGGACTGGATAACTCTGAGAAA
CACATCTAGTATAACTGAATAAGCAGAGCATCAAATTAAACAGACAGAAACCGAAAGCTCTA
TATAAATGCTCAGAGTTCTTTATGTATTTCTTATTGGCATTCAACATATGTAAATCAGAAA
ACAGGGAAATTTTCATTAAAAATATTGGTTTGAAAT

FIGURE 2

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34392

<subunit 1 of 1, 379 aa, 1 stop

<MW: 43302, pI: 7.30, NX(S/T): 1

MKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDEDNSLFPTREPR
SHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGL
TSLYGLILNNNKLTKIHPKAFLTTKKLRRLLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQ
KDTFKGMNALHVLEMSANPLDNNGIEPGAEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLD
YNKISTVELEDFKRYKELQRLGLGNKITDIENGLANIPRVREIHLENNKLKKIPSGLP
KYLQIIIFLHSNSIARVGVNDFCPTVPKMKKSLSAISLFNNPVKYWEMQPATFRCVLSRMSV
QLGNFGM

Signal sequence.

amino acids 1-15

N-glycosylation site.

amino acids 281-285

N-myristoylation sites.

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

Leucine zipper pattern.

amino acids 154-176

00943851.083001

FIGURE 3

CGGACGCGTGGGCGGACGCGTGGGCCCCGSCGACCGCCCCGGCCCCGGCCCTCCGCCCTCCGCACTCGCGCCTCC
CTCCCTCCGCCCGCTCCCGCGCCCTCCTCCCTCCCTCCTCCCCAGCTGTCCCGTTCGCGTCAATGCCGAGCCTCCC
GGCCCCGCGCGCCCGCTGCTGCTCCTCGGGCTGCTGCTGCTCGGCTCCCGGCCGGCCCCGGCGCCGGCCCCAGA
GCCCCCGTGTGCCCCATCCGTTCTGAGAAGGAGCCGCTGCCCCGTTCCGGGAGCGGCAGGCTGCACCTTCGGCGG
GAAGGTCTATGCCTTGACGAGACGTGGCACCCGGACCTAGGGCAGCCATTCCGGGGTGATGCGCTGCGTGTGTG
CGCCTGCGAGGCGCCTCAGTGGGGTCGCCGTACCAGGGGCCCTGGCAGGGTCAGCTGCAAGAACATCAAACCAGA
GTGCCCCAACCCCGGCCTGTGGGCAGCCGCGCCAGCTGCCGGGACACTGCTGCCAGACCTGCCCCAGGAGCGCAG
CAGTTCGGAGCGGCAGCCGAGCGGCCTGTCTTCGAGTATCCGCGGGACCCGGAGCATCGCAGTTATAGCGACCG
CGGGGAGCCAGGCGCTGAGGAGCGGGCCCCGTGGTGACGGCCACACGGACTTCGTGGCGCTGCTGACAGGGCCGAG
GTGCGCAGGCGGTGGCACGAGCCCCGAGTCTCGCTGCTGCGCTCTAGCCTCCGCTTCTCTATCTCCTACAGGCGGCT
GGACCGCCCTACCAGGATCCGCTTCTCAGACTCCAATGGCAGTGTCTGTTTGAGCACCCCTGCAGCCCCACCCA
AGATGGCCTGGTCTGTGGGGTGTGGCGGGCAGTGCCCTCGGTTGTCTCTGCGGCTCCTTAGGGCAGAACAGCTGCA
TGTGGCACTTGTGACACTCACTCACCTTCAGGGGAGGTCTGGGGGCCCTCATCCGGCACCGGGCCCTGGCTGC
AGAGACCTTCAGTGCCATCCTGACTCTAGAAGGCCCCCACAGCAGGGCGTAGGGGGCATCACCTGCTCACTCT
CAGTGACACAGAGGACTCCTTGCAATTTTTGCTGCTCTTCCGAGGGCTGCTGGAACCCAGGAGTGGGGGACTAAC
CCAGGTTCCCTTGAGGCTCCAGATTCTACACAGGGGCACTGCGAGAACTTCAGGCAATGTCTCAGCCCCA
GGAACCTAGGTTGCTGAGGTGCTGCCCAACCTGACAGTCCAGGAGATGGACTGGCTGGTGTGCTGGGGGAGCTGCA
GATGGCCCTGGAGTGGGCGAGGCGAGGCTGCGCATCAGTGACACATTGCTGCCAGGAAGAGCTGCGACGT
CCTGCAAAGTGTCTTTGTGGGGCTGATGCCCTGATCCAGTCCAGACGGGTGCTGCCGGCTCAGCCAGCCTCAC
GCTGCTAGGAAATGGCTCCCTGATCTATCAGGTGCAAGTGGTAGGGACAAGCAGTGAGGTGGTGGCCATGACACT
GGAGACCAAGCCTCAGCGGAGGGATCAGCGCACTGTCTGTGCCACATGGCTGGACTCCAGCCAGGAGGACACAC
GGCCGTGGGTATCTGCCCTGGGCTGGGTGCCCGAGGGGCTCATATGCTGCTGCAGAATGAGCTCTTCTGAACGT
GGGCACCAAGGACTTCCAGACGGAGAGCTTCGGGGGCACGTGGCTGCCCTGCCCTACTGTGGGCATAGCGCCCG
CCATGACACGCTGCCCCGTGCCCTAGCAGGAGCCCTGGTGCTACCCCTGTGAAGAGCCAAGCAGCAGGGCACGC
CTGGCTTTCTTGGATACCCACTGTACCTGCACATGAAGTGTGCTGGCTGGGCTGGTGGCTCAGAACAAGG
CACTGTCACTGCCCACCTCCTTGGGCCCTCCTGGAACGCCAGGGCCTCGGCGGTGCTGAAGGGATTCTATGGCTC
AGAGGCCAGGGTGTGGTGAAGGACCTGGAGCCGGAAGTGTGCGGCACCTGGCAAAGGCATGGCCTCCCTGAT
GATCACCAACCAAGGGTAGCCCCAGAGGGGAGCTCCGAGGGCAGGTGCACATAGCCAACCAATGTGAGGTTGGCGG
ACTGCGCCTGGAGGCGGCCGGGGCCGAGGGGGTGCGGGCGCTGGGGGCTCCGGATACAGCCTCTGCTGCGCCGCC
TGTGGTGCCTGGTCTCCCGGCCCTAGCGCCCGCCAAACCTGGTGGTCTGGGCGGCCCGAGACCCCAACACATG
CTTCTTCGAGGGGCAGCAGCGCCCCACGGGGCTCGCTGGGCGCCCAACTACGACCCGCTCTGCTCACTCTGCAC
CTGCCAGAGACGAACGGTGATCTGTGACCCGGTGGTGTGCCACCGCCAGCTGCCACACCCGGTGCAGGCTCC
CGACCACTGCTGCCCTGTTTGCCCTGAGAAACAAGATGTGAGAGACTTGCCAGGGCTGCCAAGGAGCCGGGACCC
AGGAGAGGGCTGCTATTTTGATGGTGACCGGAGCTGGCGGGCAGCGGGTACGCGGTGGCACCCCGTTGTGCCCC
CTTTGGCTTAATTAAGTGTGCTGTCTGCACCTGCAAGGGGGGCACTGGAGAGGTGCACGTGTGAGAAGGTGCAGTG
TCCCCGGCTGGCCTGTGCCAGCCTGTGCGTGTCAACCCACCGACTGCTGCAAACAGTGTCCAGTGGGGTCGGG
GGCCCCACCCCACTGAGGGGACCCCATGCAGGCTGATGGGCCCCGGGGCTGCCGTTTTGCTGGGCAGTGGTTCCC
AGAGAGTCAGAGCTGGCACCCCTCAGTGCCCCCTTTTGGAGAGATGAGCTGTATCACCTGCAGATGTGGGGCAGG
GGTGCCTCACTGTGAGCGGGATGACTGTTCACTGCCACTGTCTGTGGCTCGGGGAAGGAGAGTCGATGCTGTTC
CCGCTGCACGGCCACCGCGGCCCCAGAGACCAGAACTGATCAGAGCTGGAGAAAGAAGCCGAAGGCTCTTA
GGGAGCAGCCAGAGGGCCAAGTGACCAAGAGGATGGGGCTGAGCTGGGGAAGGGGTGGCATCGAGGACCTTCTT
GCATTCTCCTGTGGGAAGCCAGTGCCTTTGCTCCTCTGTCTGCTCTACTCCCACCCCACTACCTCTGGGAA
CCACAGCTCCACAAGGGGGAGAGGCAGCTGGGCCAGACCGAGGTACAGCCACTCCAAGTCTGCCCTGCCACCC
TCGGCCTCTGTCTGGAAGCCCCACCCCTTTCTCCTGTACATAATGTCACTGGCTTGTGGGATTTTAATTTA
TCTTCACTCAGACCAAGGGCCCCGACACTCCACTCCTGCTGCCCTGAGCTGAGCAGAGTCATTATTGGAGAG
TTTTGTATTTATTAAACATTTCTTTTTCAGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 4

><subunit 1 of 1, 954 aa, 1 stop

><MW: 101960, pI: 8.21, NX(S/T): 5

MPSLPAPPAPLLLLLGLLLLGSRPARGAGPEPPVLPIRSEKEPLPVRGAAGCTFGGKVYALDE
TWHPDLGQPFQVMRCVLCACEAPQWGRRTGRPGRVSCNIKPECPTPACGQPRQLPGHCCQT
CPQERSSSERQPSGLSFEYPRDPEHRSSDRGEPGAEERARGDGHTDFVALLTGPRSQAVAR
ARVSLRSSLRFSISYRRLDRPTRIRFSDSNGSVLFEHPAAPTQDGLVCGVWRAVPRLSLRL
LRAEQLHVALVTLTHPSGEVWGPLIRHRALAAETFSAILTLEGPPQQGVGGITLLTSLDTE
SLHFLLLFRGLLEPRSGGLTQVPLRLQILHQGQLLRELQANVSAQEPGFAEVLPLNLTVQEMD
WLVLGELQMALEWAGRPGRLRISGHIAARKSCDVLQSVLCGADALIPVQTGAAGSASLTLLGN
GSLIYQVQVVGTSSEVVAMTLETKPQRRDQRTVLCHMAGLQPGGHTAVGICPGLGARGAHML
LQNELFLNVGTKDFPDGELRGHVAALPYCGHSARHDTLPVPLAGALVLPVKSQAAGHAWLS
LDTHCHLHYEVLLAGLGGSEQGTVAHLLGPPGTPGPRLLKGFYQSEAQGVVKDLEPELLR
HLAKGMASLMITTKGSPRGELRGQVHIANQCEVGGLRLEAAGAEGVRALGAPDTASAAPPVV
PGLPALAPAKPGGPRPRDNTCCFEGQQRPHGARWAPNYDPLCSLCTCQRRTVICDPVVC
PPSCPHPVQAPDQCCPVCPEKQDVRDLPLPRSRDPGEGCYFDGDRSWRAAGTRWHPVVPF
GLIKCAVCTCKGGTGEVHCEKVQCPRLACAQPVVNPTDCCKQCPVGSAGHPQLGDPMQADG
PRGCRFAGQWFPESQSWHPSVPPFGEMSCITCRGAGVPHCERDDCSLPLSCGSGKESRCCS
RCTAHRPPETRTDPELEKEAEGS

Signal sequence.

amino acids 1-23

N-glycosylation sites.

amino acids 217-221, 351-355, 365-369, 434-438

Tyrosine kinase phosphorylation sites.

amino acids 145-153, 778-786

N-myristoylation sites.

amino acids 20-26, 47-53, 50-56, 69-75, 73-79, 232-238, 236-242,
390-396, 422-428, 473-479, 477-483, 483-489, 489-495, 573-579,
576-582, 580-586, 635-641, 670-676, 773-779, 807-813, 871-877,
905-911

Amidation site.

amino acids 87-91

Cell attachment sequence.

amino acids 165-168

Leucine zipper pattern.

amino acids 315-337

09943851-083004

FIGURE 5

GGCGGAGCAGCCCTAGCCGCCACCGTCGCTCTCGCAGCTCTCGTCGCCACTGCCACCGCCGCCGCCGTCCTACTGCG
TCCTGGCTCCGGCTCCCGCGCCCTCCCGGCCGCGCCATGCAGCCCCGCGCGCCAGGCGCCCGGTGCGCAGCTGC
TGCCCGCGCTGGCCCTGCTGCTGCTGCTGCTCGGAGCGGGGCCCGAGGCAGCTCCCTGGCCAAACCCGGTGCCCG
CCGCGCCCTTGTCTGCGCCCGGGCCGTGCGCCGCGCAGCCCTGCCGGAATGGGGGTGTGTGCACCTCGCGCCCTG
AGCCGGACCCGAGCACC CGGCCCGCCGCGAGCCTGGCTACAGCTGCACCTGCCCCGCCGGGATCTCCGGCG
CCAACCTGCCAGCTTGTTCAGATCCTTGTGCCAGCAACCCTTGTACCATGGCAACTGCAGCAGCAGCAGCAGCA
GCAGCAGCGATGGCTACCTCTGCATTTGCAATGAAGGCTATGAAGGTCCCAACTGTGAACAGGCACCTTCCCAGTC
TCCCAGCCACTGGCTGGACCGAATCCATGGCACCCCGACAGCTTCAGCCTGTTCTCTGCTACTCAGGAGCCTGACA
AAATCCTGCCTCGCTCTCAGGCAACGGTGACACTGCCTACCTGGCAGCCGAAAAACAGGGCAGAAAGTTGTAGAAA
TGAAATGGGATCAAGTGGAGGTGATCCAGATATTGCCCTGTGGGAATGCCAGTTCTAACAGCTCTGCGGGTGGCC
GCCTGGTATCCTTTGAAGTGCCACAGAACACCTCAGTCAAGATTGCGCAAGATGCCACTGCCTCAGTATTGTTGC
TCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAGTGTGACCCCTTCAGGCTT
CAGGGGGACTGGTCTCTCTGGAGGAGATGCTCGCCTTGGGGAATAATCACTTTATTGGTTTTGTGAATGATTCTG
TGACTAAGTCTATTGTGGCTTTGCGCTTAACCTCTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCAG
CAAATGACTTGGAGTGTTT CAGGAAAAGGAAAATGCACCACGAAGCCGTGAGAGGCAACTTTTTCTGTACCTGTG
AGGAGCAGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAACGCGAGCT
GTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTTGCCTTCTGGTTATACTGGAGAGCTTT
GCCAGTCCAAGATTGATTACTGCATCCTAGACCCATGCAGAAATGGAGCAACATGCATTTCCAGTCTCAGTGGAT
TCACCTGCCAGTGTCCAGAAGGATACTTCGGATCTGCTTGTGAAGAAAAGGTGGACCCCTGCGCCTCGTCTCCGT
GCCAGAACAACGGCACCTGCTATGTGGACGGGGTACACTTTACCTGCAACTGCAGCCCGGGCTTCACAGGGCCGA
CCTGTGCCAGCTTATTGACTTCTGTGCCCTCAGCCCTGTGCTCATGGCACGTGCCGACGCTGGGCACCAGCT
ACAAATGCCTCTGTGATCCAGGTTACCATGGCCTCTACTGTGAGGAGGAATATAATGAGTGCCTCTCCGCTCCAT
GCCTGAATGCAGCCACCTGCAGGGACCTCGTTAATGGCTATGAGTGTGTGTGCTGGCAGAAATACAAAGGAACAC
ACTGTGAATTGTACAAGGATCCCTGCGCTAACGTCAGCTGTCTGAACGGAGCCACCTGTGACAGCGACGGCCTGA
ATGGCACGTGCATCTGTGCACCCGGGTTTACAGGTGAAGAGTGCGACATTGACATAAATGAATGTGACAGTAACC
CCTGCCACCATGGTGGGAGCTGCCTGGACCGCCCAATGGTTATAACTGCCACTGCCCGCATGGTTGGGTGGGAG
CAAACCTGTGAGATCCACCTCCAATGGAAGTCCGGGCACATGGCGGAGAGCCTCACCAACATGCCACGGCACTCCC
TCTACATCATCATTGGAGCCCTCTGCGTGGCCTTCATCCTTATGCTGATCATCTGATCGTGGGGATTGCGCGCA
TCAGCCGCATTGAATACCAGGGTTCTTCCAGGCCAGCCTATGAGGAGTTCTACAAC TGCCGACGATCGACAGCG
AGTTCAGCAATGCCATTGCATCCATCCGGCATGCCAGGTTTGGAAGAAATCCCGGCCTGCAATGTATGATGTGA
GCCCCATCGCCTATGAAGATTACAGTCCTGATGACAAACCCTTGGTCACACTGATTAAAAC TAAAGATTTGTAAT
CTTTTTTTGGATTATTTTTCAAAAAGATGAGATACTACACTCATTTAAATATTTTTAAGAAAATAAAAAGCTTAA
GAAATTTAAATGCTAGCTGCTCAAGAGTTTTTCAGTAGAATATTTAAGAACTAATTTTCTGCAGCTTTTAGTTTG
GAAAAATATTTTTAAAAACAAAATTTGTGAAACCTATAGACGATGTTTTAATGTACCTTCAGCTCTCTAACTGT
GTGCTTCTACTAGTGTGTGCTCTTTTCACTGTAGACACTATCACGAGACCCAGATTAATTTCTGTGGTTGTTACA
GAATAAGTCTAATCAAGGAGAAGTTTCTGTTTTGACGTTTGAGTGCCGGCTTCTGAGTAGAGTTAGGAAAACCAC
GTAACGTAGCATATGATGTATAATAGAGTATACCCGTTACTTAAAAAGAAGTCTGAAATGTTTCGTTTTGTGAAA
AGAACTAGTTAAATTTACTATTCTTAACCCGAATGAAATTAGCCTTTGCCTTATTCTGTGCATGGGTAAGTAAC
TTATTTCTGCACTGTTTTGTGAACTTTGTGGAAACATTCTTTCGAGTTGTTTTTGTCAATTTTCGTAACAGTCG
TCGAACTAGGCCTCAAAAACATACGTAACGAAAAGGCCTAGCGAGGCAAATCTGATTGATTTGAATCTATATTT
TTCTTTAAAAAGTCAAGGGTTCTATATTGTGAGTAAATTAATTTACATTTGAGTTGTTTGTGCTAAGAGGTAG
TAAATGTAAGAGAGTACTGGTTCCTTCAGTAGTGAGTATTTCTCATAGTGCAGCTTTATTTATCTCCAGGATGTT
TTTGTGGCTGTATTTGATTGATATGTGCTTCTTCTGATTCTTGCTAATTTCCAACCATATTGAATAAATGTGATC
AAGTCA

FIGURE 6

><subunit 1 of 1, 737 aa, 1 stop

><MW: 78475, pI: 5.09, NX(S/T): 11

MQPRRAQAPGAQLLPALALLLLLLGAGPRGSSLANPVPAAPLSAPGPCAAQPCRNGGVCTSR
PEPDPQHPAPAGEPGYSCTCPAGISGANQQLVADPCASNPCHHGNCSSSSSSSSSDGYLCICN
EGYEGPNCEQALPSLPATGWTESMAPRQLQVPVATQEPDKILPRSQATVTLPTWQPKTGQKV
VEMKWDQVEVIPDIACGNASSNSSAGGRLVSFEVPQNTSVKIRQDATASLILLWKVTATGFQ
QCSLIDGRSVTPLQASGGLVLEEMLALGNNHFIGFVNDSVTKSIVALRLTLVVKVSTCVPG
ESHANDLECSGKGKCTTKPSEATFSTCEEQYVGTFCEEYDACQRKPCQNNASCIDANEKQD
GSNFTCVCLPGYTGELCQSKIDYCIDPCRNGATCISLSSGFTCCPEGYFGSACEEKVDPC
ASSPCQNNGTCTYVDGVHFTCNCSPGFTGPTCAQLIDFCALSPCAHGTCRSVGTSYKCLCDPG
YHGLYCEEEYNECLSAAPCLNAATCRDLVNGYECVCLAELYKGTCELKDPKANVSCLNGATC
DSDGLNGTCTICAPGFTGEECDIDINECDSPNCHGGSCLDQPNGYNCHCPHGWWGANCEIHL
QWKSGHMAESLTNMPRHSLYIIIGALCVAFILMLIILIVGICRISRIEYQGSSRPAYEEFYN
CRSIDSEFSNAIASIRHARFGKSRPAMYDVSPAIYEDYSPDDKPLVTLIKTKDL

Signal sequence.

amino acids 1-28

Transmembrane domain.

amino acids 641-660

N-glycosylation sites.

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,
375-379, 442-446, 549-553, 564-568

Glycosaminoglycan attachment site.

amino acids 320-324

Tyrosine kinase phosphorylation sites.

amino acids 490-498, 674-682

N-myristoylation sites.

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,
373-379, 449-455, 480-486, 562-568, 565-571

Amidation site.

amino acids 702-706

Aspartic acid and asparagine hydroxylation site.

amino acids 520-532, 596-608

EGF-like domain cysteine pattern signatures.

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,
491-503, 529-541, 567-579, 605-617

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FIGURE 7

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTTCAGGCTTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA
ATCACTTTATTGGTTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAACT
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTTT
AGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTTCTGTACCTGTGAGGAGC
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCC
TGGTTATACTGGAGAGCTTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGGAG

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100E80" T58E4660

FIGURE 8

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTTCAGGCTTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA
ATCACTTTATTGGTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAACT
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTTT
AGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTTCCTGTACCTGTGAGGAGC
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCC
TGGTTATACTGGAGAGCTTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGGAG

0943351.083001

FIGURE 9

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCTCCAGCCTGTAACCTGTGCCTACACCACGCCAG
GCCCCCCCAGAGCCCTCACCACGCTGGGCGCCCCAGAGCCCACACCATGCCGGGCACCTAC
GCTCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGGCCCT
GATGCGGGACTTCCCGCTCGTGGACGGCCACAACGACCTGCCCCTGGTCCTAAGGCAGGTTT
ACCAGAAAGGGCTACAGGATGTTAACCTGCGCAATTTACGCTACGGCCAGACCAGCCTGGAC
AGGCTTAGAGATGGCCTCGTGGGCGCCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCA
GGACCGGGATGCCCTGCGCCTCACCTGGAGCAGATTGACCTCATA CGCCGCATGTGTGCCT
CCTATTCTGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCC
TGCTTCATCGGTGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTT
CTACATGCTGGGAGTGCCTACCTGACGCTCACCCACACCTGCAACACACCCTGGGCAGAGA
GCTCCGCTAAGGGCGTCCACTCCTTCTACAACAACATCAGCGGGCTGACTGACTTTGGTGAG
AAGGTGGTGGCAGAAATGAACCGCCTGGGCATGATGGTAGACTTATCCCATGTCTCAGATGC
TGTGGCACGGCGGGCCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCCACTCGGCTGCCC
GGGGTGTGTGCAACAGTGCTCGGAATGTTCTGATGACATCCTGCAGCTTCTGAAGAAGAAC
GGTGGCGTCGTGATGGTGTCTTTGTCCATGGGAGTAATACAGTGCAACCCATCAGCCAATGT
GTCCACTGTGGCAGATCACTTCGACCACATCAAGGCTGTCATTGGATCCAAGTTCATCGGGA
TTGGTGGAGATTATGATGGGGCCGGCAAATTCCTCAGGGGCTGGAAGACGTGTCCACATAC
CCGGTCCTGATAGAGGAGTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCTT
TCGTGGAAACCTGCTGCGGGTCTTCAGACAAGTGGAAGGTACAGGAAGAAAACAAATGGC
AAAGCCCCTTGAGGACAAGTTCCCGGATGAGCAGCTGAGCAGTTCTTGCCACTCCGACCTC
TCACGTCTGCGTCAGAGACAGAGTCTGACTTCAGGCCAGGAACTCACTGAGATTCCCATACA
CTGGACAGCCAAGTTACCAGCCAAGTGGTCAGTCTCAGAGTCCTCCCCCACATGGCCCCAG
TCCTTGCAAGTTGTGGCCACCTTCCCAGTCCTTATTCTGTGGCTCTGATGACCCAGTTAGTCC
TGCCAGATGTCACTGTAGCAAGCCACAGACACCCCAAAAGTTCCCCTGTTGTGCAGGCACA
AATATTTCTGAAATAAATGTTTTGGACATAG

05943851.083001

FIGURE 10

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35595

<subunit 1 of 1, 433 aa, 1 stop

<MW: 47787, pI: 6.11, NX(S/T): 5

MPGTYAPSTTLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIIRMCASYSELELVTSAKALND
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYPVLIEELLSRGWSEEEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS
CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHMAPVLAVVATFPVLILWL

N-glycosylation sites.

amino acids 58-62, 123-127, 182-186, 273-277

N-myristoylation sites.

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

Renal dipeptidase active site.

amino acids 134-157

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FIGURE 11

AAAACCTATAAATATTCCGGATTATTCATACCGTCCCACCATCGGGCGCGGATCCGCGGCCG
CGAATTCTAAACCAACATGCCGGGCACCTACGCTCCCTCGACCACACTCAGTAGTCCCAGCA
CCCAGGGCCTGCAAGAGCAGGCACGGGCCCTGATGCGGGACTTCCCGCTCGTGGACGGCCAC
AACGACCTGCCCCTGGTCCTAAGGCAGGTTTACCAGAAAGGGCTACAGGATGTTAACCTGCG
CAATTTAGCTACGGCCAGACCAGCCTGGACAGGCTTAGAGATGGCCTCGTGGGCGCCCAGT
TCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCGGGATGCCCTGCGCCTCACCCCTGGAG
CAGATTGACCTCATACGCCGCATGTGTGCCTCCTATTCTGAGCTGGAGCTTGTGACCTCGGC
TAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCATCGGTGTAGAGGGTGGCCACTCGC
TGGACAATAGCCTCTCCATCTTACGTACCTTCTACATGCTGGGAGTGGCTACCTGACGCTC
ACCCACACCTGCAACACACCCTGGGCAGAGAGCTCCGCTAAGGGCGTCCACTCCTTCTACAA
CAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGTGGCAGAAATGAACCGCCTGGGCA
TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCGGGCCCTGGAAGTGTACAG
GCACCTGTGATCTTCTCCCACTCGGCTGCCCCGGGTGTGTGCAACAGTGCTCGGAATGTTCC
TGATGACATCCTGCAGCTTCTGAAGAAGAACGGTGGCGTCGTGATGGTGTCTTTGTCCATGG
GAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGATCACTTCGACCACATC
AAGGCTGTCATTGGATCCAAGTTCATCGGGATTGGTGGAGATTATGATGGGGCCGGCAAATT
CCCTCAGGGGCTGGAAGACGTGTCCACATACCCGGTCCCTGATAGAGGAGTTGCTGAGTCGTG
GCTGGAGTGAGGAAGAGCTTCAGGGTGTCTTCGTGGAAACCTGCTGCGGGTCTTCAGACAA
GTGGAAAAGGTACAGGAAGAAAACAAATGGCAAAGCCCCCTTGAGGACAAGTTCCCGGATGA
GCAGCTGAGCAGTTCTTGCCACTCCGACCTCTCACGTCTGCGTCAGAGACAGAGTCTGACTT
CAGGCCAGGAACTCACTGAGATTCCCATACTGGACAGCCAAGTTACCAGCCAAGTGGTCA
GTCTCAGAGTCCTCCCCCACCCTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGA
ACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCAAACCCAAGGACACC

094354-0304

FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA35872

><subunit 1 of 1, 446 aa, 0 stop

><NX(S/T): 5

MPGTYAPSTTLSSPSTQGLQEQARALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIIRMCASYSELELVTSAKALND
TQKLACLIQVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYPVLIEELLSRGWSEEEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS
CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHDPDKTHTCPPCPAPELLGGP
SVFLFPPKPKDT

0943851.083001

FIGURE 13

CGCCAGCGACGTGCGGGCGGCCTGGCCCCGCGCCCTCCCGCGCCCGGCCTGCGTCCCGCGCC
CTGCGCCACCGCCGCGCGAGCCGAGCCCGCCGCGCGCCCCGGCAGCGCCGGCCCCATGCCC
GCCGGCCGCGGGGGCCCCGCGCCCAATCCGCGCGGCGGCCGCGCCGCTTGCTGCCCCCTGCT
GCTGCTGCTCTGCGTCCTCGGGGCGCCGCGAGCCGGATCAGGAGCCCACACAGCTGTGATCA
GTCCCCAGGATCCCACGCTTCTCATCGGCTCCTCCCTGCTGGCCACCTGCTCAGTGCACGGA
GACCCACCAGGAGCCACCGCCGAGGGCCTCTACTGGACCCTCAACGGGCGCCGCCTGCCCCC
TGAGCTCTCCCGTGTA CTCAACGCCTCCACCTTGGCTCTGGCCCTGGCCAACCTCAATGGGT
CCAGGCAGCGGTGCGGGGACAACCTCGTGTGCCACGCCC GTGACGGCAGCATCCTGGCTGGC
TCCTGCCTCTATGTTGGCCTGCCCCAGAGAAACCCGTCAACATCAGCTGCTGGTCCAAGAA
CATGAAGGACTTGACCTGCCGCTGGACGCCAGGGGCCCACGGGGAGACCTTCCTCCACACCA
ACTACTCCCTCAAGTACAAGCTTAGGTGGTATGGCCAGGACAACACATGTGAGGAGTACCAC
ACAGTGGGGCCCCACTCCTGCCACATCCCCAAGGACCTGGCTCTCTTTACGCCCTATGAGAT
CTGGGTGGAGGCCACCAACCGCCTGGGCTCTGCCCCGCTCCGATGTA CTACGCTGGATATCC
TGGATGTGGTGACCACGGA CCCCCCGCCCGACGTGCACGTGAGCCGCGTCCGGGGCCTGGAG
GACCAGCTGAGCGTGCGCTGGGTGTGCGCACCCGCCCTCAAGGATTTCTCTTTCAAGCCAA
ATACCAGATCCGCTACCGAGTGGAGGACAGTGTGGACTGGAAGGTGGTGGACGATGTGAGCA
ACCAGACCTCCTGCCGCCTGGCCGGCCTGAAACCCGGCACCGTGTACTTCGTGCAAGTGCGC
TGCAACCCCTTTGGCATCTATGGCTCCAAGAAAGCCGGGATCTGGAGTGAGTGGAGCCACCC
CACAGCCGCCTCCACTCCCCGAGTGAGCGCCCGGGCCCCGGCGGGCGGGGGCGTGCGAACCGC
GGGGCGGAGAGCCGAGCTCGGGGCCGTGCGGCGCGAGCTCAAGCAGTTCTCTGGGCTGGCTC
AAGAAGCACGCGTACTGCTCCAACCTCAGCTTCCGCCTCTACGACCAGTGGCGAGCCTGGAT
GCAGAAGTCGCACAAGACCCGCAACCAGGACGAGGGGATCCTGCCCTCGGGCAGACGGGGCA
CGGCGAGAGGTCCTGCCAGATTAAGCTGTAGGGGCTCAGGCCACCCTCCCTGCCACGTGGAGA
CGCAGAGGCCGAACCCAAACTGGGGCCACCTCTGTACCCTCACTTCAGGGCACCTGAGCCAC
CCTCAGCAGGAGCTGGGGTGGCCCCCTGAGCTCCAACGGCCATAACAGCTCTGACTCCCACGT
GAGGCCACCTTTGGGTGCACCCAGTGGGTGTGTGTGTGTGTGTGAGGGTTGGTTGAGTTGC
CTAGAACCCCTGCCAGGGCTGGGGGTGAGAAGGGGAGTCATTACTCCCCATTACCTAGGGCC
CCTCCAAAAGAGTCCTTTTAAATAAATGAGCTATTTAGGTGCTGTGATTTGTGAAAAAAAAA
AAA

05943851.033001

FIGURE 14

><ss.DNA38113

><subunit 1 of 1, 422 aa, 1 stop

><MW: 46302, pI: 9.42, NX(S/T): 6

MPAGRRGPAAQSARRPPPLLPLLLLLCVLGAPRAGSGAHTAVIS PQDPTLLIGSSLLATCSV
HGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQSRSGDNLVCHARDGSIL
AGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYS LKYKLRWYGQDNTCEE
YHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTDPDPPDVHVS RVGG
LEDQLSVRWVSP PALKDFLFQAKYQIRYRVEDSV DWKVDDVSNQTSCRLAGLKPGTVYFVQ
VRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSSGPVRRELKQFLG
WLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGPAR

Signal sequence.

amino acids 1-30

Transmembrane domain.

amino acids 44-61

N-glycosylation sites.

amino acids 92-96, 104-108, 140-144, 168-172, 292-296, 382-386

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 413-417

N-myristoylation sites.

amino acids 30-36, 37-43, 73-79, 121-127, 179-185, 218-224,
300-306, 317-323, 320-326, 347-353, 355-361, 407-413

Amidation site.

amino acids 3-7, 79-83, 411-415

Growth factor and cytokines receptors family signature 2.

amino acids 325-331

0943851.083001
FOOESD-TSSE7660

FIGURE 15

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA
AAAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTTCGTGAAGCTTTTTATTCTTAA
GAGGAGAAAATCAGTCACCGGCGAAATCGTGCTGATTACAGGAGCTGGGCATGGAATTGGGA
GACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTTCTCTGGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTTACATACCTTTGT
GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGACATTTCTGGACTACAAA
GGCATTCTTCTTCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG
CTGGACATGTCTCGGTCCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGCTGCTGTTGGA
TTTCATAAACTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG
TCTGTGTCCTAATTTTCGTAAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG
ATTTTTATTCCATCTTCTATAGCTTTTTTAACAACATTGGAAAGGATCCTTCCTGAGCGTTT
CCTGGCAGTTTTTAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA
AAGCGCAATAAGCACCTAGTTTTCTGAAAACCTGATTTACCAGGTTTAGGTTGATGTCATCTA
ATAGTGCCAGAATTTTAATGTTTGAACCTCTGTTTTTTCTAATTATCCCCATTTCTTCAATA
TCATTTTTGAGGCTTTGGCAGTCTTCATTTACTACCACTTGTTCTTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAA
CCAAAATGACTTTATTAAAATAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA
AATTTGTACCATAACCGTTTATTTAACATATATTTTTATTTTTTGATTGCACTTAAATTTTGT
ATAATTTGTGTTTCTTTTTCTGTTCTACATAAAATCAGAACTTCAAGCTCTCTAAATAAAA
TGAAGGACTATATCTAGTGGTATTTTACAATGAATATCATGAACTCTCAATGGGTAGGTTTC
ATCCTACCCATTGCCACTCTGTTTCCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT
GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTTAAG
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA
AA
AA

0943851-083001

09-03-108306

<subunit 1 of 1, 300 aa, 1 stop

MKFLLDI L L L L P L L I V C S L E S F V K L F I P K R R K S V T G E I V L I T G A G H G I G R L T A Y E F A K L K S K
 L V L W D I N K H G L E E T A A K C K G L G A K V H T F V V D C S N R E D I Y S S A K K V K A E I G D V S I L V N N A G V V
 Y T S D L F A T Q D P Q I E K T F E V N V L A H F W T T K A F L P A M T K N N H G H I V T V A S A A G H V S V P F L L A Y C
 S S K F A A V G F H K T L T D E L A A L Q I T G V K T T C L C P N F V N T G F I K N P S T S L G P T L E P E E V N R L M H
 G I L T E O K M I F I P S S I A F L T T L E R I L P E R F L A V L K R K I S V K F D A V I G Y K M K A Q

amino acids 1-19

amino acids 170-187

amino acids 30-34, 283-287

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 17

GACTAGTTCTCTTGGAGTCTGGGAGGAGGAAAGCGGAGCCGGCAGGGAGCGAACCAGGACTG
GGGTGACGGCAGGGCAGGGGGCGCCTGGCCGGGGAGAAGCGCGGGGGCTGGAGCACCACCAA
CTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGGACT
GCGAGAGGACCCCGGCGTCCGGGGCTCCCGGTGCCAGCGCTATGAGGCCACTCCTCGTCCTGC
TGCTCCTGGGCCTGGCGGGCCGGCTCGCCCCCACTGGACGACAACAAGATCCCCAGCCTCTGC
CCGGGGCACCCTGGCCTTCCAGGCACGCCGGGCCACCATGGCAGCCAGGGCTTGCCGGGGCCG
CGATGGCCGCGACGGCCGCGACGGCGCGCCCGGGGCTCCGGGAGAGAAAGGCGAGGGCGGGA
GGCCGGGACTGCCGGGACCTCGAGGGGACCCCGGGCCGCGAGGAGAGGCGGGACCCGCGGGG
CCCACCGGGCCTGCCGGGGAGTGCTCGGTGCCTCCGCGATCCGCCTTCAGCGCCAAGCGCTC
CGAGAGCCGGGTGCCTCCGCCGTCTGACGCACCCTTGCCCTTCGACCGCGTGCTGGTGAACG
AGCAGGGACATTACGACGCCGTACCGGCAAGTTCACCTGCCAGGTGCCTGGGGTCTACTAC
TTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAATGGCGA
ATCCATTGCCTCTTTCTTCCAGTTTTTCGGGGGGTGGCCCAAGCCAGCCTCGCTCTCGGGGG
GGGCCATGGTGAGGCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTAC
ATTGGCATCTATGCCAGCATCAAGACAGACAGCACCTTCTCCGGATTTCTGGTGTACTCCGA
CTGGCACAGCTCCCCAGTCTTTGCTTAGTGCCCACTGCAAAGTGAGCTCATGCTCTCACTCC
TAGAAGGAGGGTGTGAGGCTGACAACCAGGTCATCCAGGAGGGCTGGCCCCCCTGGAATATT
GTGAATGACTAGGGAGGTGGGGTAGAGCACTCTCCGTCTGCTGCTGGCAAGGAATGGGAAC
AGTGGCTGTCTGCGATCAGGTCTGGCAGCATGGGGCAGTGGCTGGATTTCTGCCCAAGACCA
GAGGAGTGTGCTGTGCTGGCAAGTGTAAGTCCCCAGTTGCTCTGGTCCAGGAGCCCACGGT
GGGGTGCTCTCTTCTGGTCCTCTGCTTCTCTGGATCCTCCCCACCCCTCCTGCTCCTGGG
GCCGGCCCTTTTCTCAGAGATCACTCAATAAACCTAAGAACCCTCATAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

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FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40592

><subunit 1 of 1, 243 aa, 1 stop

><MW: 25298, pI: 6.44, NX(S/T): 0

MRPLLVLALLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAP
GEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSKRSESRVPPPSDAPLP
FDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWP
KPASLSGGAMVRLEPEDQVWVQVGVDYIGIYASIKTDSTFSGFLVYSDWHSSPVFA

Signal sequence.

amino acids 1-15

N-myristoylation sites.

amino acids 11-17, 68-74, 216-222

Cell attachment sequence.

amino acids 77-80

094351-083001
T00E80-T58E4650

FIGURE 19

CTCTTTTGTCCACCAGCCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTGAG
AAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCCCAACAGACCCAT
GCTGCATCCAGAGACCTCCCCTGGCCGGGGGCATCTCCTGGCTGTGCTCCTGGCCCTCCTTG
GCACCACCTGGGCAGAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC
CTGAACAGGAAGGAGAGTTTCTTGCTCCTCTCCCTGCACAACCGCCTGCGCAGCTGGGTCCA
GCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCCAACTGGCTCAAG
CCAGGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCCCTG
CAAGTGGGCTGGAACATGCAGCTGCTGCCCCGCGGGCTTGCGCTCCTTTGTTGAAGTGGTCAG
CCTATGGTTTGCAGAGGGGCAGCGGTACAGCCACGCGGCAGGAGAGTGTGCTCGCAACGCCA
CCTGCACCCACTACACGCAGCTCGTGTGGGCCACCTCAAGCCAGCTGGGCTGTGGGCGGCAC
CTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCTGTGCCTACTCCCCGGAGGCAA
CTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGAAGGGTGCCTGGTGTTCGCTCTGCA
CAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCATGCAGGGGGGCTCTGTGAGGTCCCC
AGGAATCCTTGTGCGATGAGCTGCCAGAACCATGGACGTCTCAACATCAGCACCTGCCACTG
CCACTGTCCCCCTGGCTACACGGGCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTGTGC
ACGGCCGGTTCCGGGAGGAGGAGTGCTCGTGCGTCTGTGACATCGGCTACGGGGGAGCCCAG
TGTGCCACCAAGGTGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTT
CATGGTGTCTTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAAGGCG
GGGTGCTGGCCCAGATCAAGAGCCAGAAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCGC
CTGGAGACCACCAACGAGGTGACTGACAGTGAAGTTCGAGACCAGGAACCTTCTGGATCGGGCT
CACCTACAAGACCGCCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTACCA
GTTTTGCCTTTGGGCAGCCTGACAACACCGGGCTGGTGTGGCTGAGTGCTGCCATGGGGTTT
GGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAAAC
CCGAAACCGTTACATCTGCCAGTTTGCCCAGGAGCACATCTCCCGGTGGGGCCCAGGGTCCT
GAGGCCTGACCACATGGCTCCCTCGCCTGCCCTGGGAGCACCGGCTCTGCTTACCTGTCTGC
CCACCTGTCTGGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGA
CCTTGCACAATGCCAGAAGTTGGGCAGAGAGAGGCAGGGAGGCCAGTGAGGGCCAGGGAGTG
AGTGTTAGAAGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGA
TGGCGAAGGAGAGGACACCGCCAGTGGTCCAAAAGGCTGCTCTCTTCCACCTGGCCCAGAC
CCTGTGGGGCAGCGGAGCTTCCCTGTGGCATGAACCCACGGGGTATTAAATTATGAATCAG
CTGAAAAAAAAAAAAA

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FIGURE 20

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44176

<subunit 1 of 1, 455 aa, 1 stop

<MW: 50478, pI: 8.44, NX(S/T): 2

MLHPETSPGRGHELLAVLLALLGTTWAEVWPPQLQEAPMAGALNRKESFLLLSLHNRLRSWV
QPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVV
SLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVCAYSPGG
NWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHGRLNISTCH
CHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFHTCDLRIDGDC
FMVSSEADTYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLTNEVTDSDFETRNFNFWIG
LTYKTAKDSFRWATGEHQAFSTFAFGQPDNHGLVWLSAAMGFGNCVELQASAAFNWNDQRCK
TRNRYICQFAQEHISRWGPGS

Signal sequence.

amino acids 1-26

Transmembrane domain.

amino acids 110-124

N-glycosylation sites.

amino acids 144-148, 243-247

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 45-49

N-myristoylation sites.

amino acids 22-28, 99-105, 131-137, 201-207, 213-219, 287-293,
288-294, 331-337, 398-404

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 204-215

EGF-like domain cysteine pattern signature.

amino acids 249-261, 280-292

C-type lectin domain signature.

amino acids 417-442

FIGURE 21

CGGACGCGTGGGCTGGGCGCTGCAAAGCGTGTCCCGCCGGGTCCCCGAGCGTCCCGCGCCCT
CGCCCCGCCATGCTCCTGCTGCTGGGGCTGTGCCTGGGGCTGTCCCTGTGTGTGGGGTTCGCA
GGAAGAGGCGCAGAGCTGGGGCCACTCTTCGGAGCAGGATGGACTCAGGGTCCCGAGGCAAG
TCAGACTGTTGCAGAGGCTGAAAACCAAACCTTTGATGACAGAATTCTCAGTGAAGTCTACC
ATCATTTCCTCGTTATGCCTTCACTACGGTTTCTGCGAGAATGCTGAACAGAGCTTCTGAAGA
CCAGGACATTGAGTTCAGATGCAGATTCCAGCTGCAGCTTTCATCACCAACTTCACTATGC
TTATTGGAGACAAGGTGTATCAGGGCGAAATTACAGAGAGAGAAAAGAAGAGTGGTGATAGG
GTAAAAGAGAAAAGGAATAAAACCAAGAAATGGAGAGAAGGGGACTGAAATATTCAG
AGCTTCTGCAGTGATTCCCAGCAAGGACAAAGCCGCTTTTTCTGAGTTATGAGGAGCTTC
TGCAGAGGCGCCTGGGCAAGTACGAGCACAGCATCAGCGTGCGGCCCCAGCAGCTGTCCGGG
AGGCTGAGCGTGGACGTGAATATCCTGGAGAGCGCGGGCATCGCATCCCTGGAGGTGCTGCC
GCTTCACAACAGCAGGCAGAGGGGCAGTGGGCGCGGGGAAGATGATTCTGGGCCTCCCCCAT
CTACTGTCATTAACCAAAATGAAACATTTGCCAACATAATTTTTAAACCTACTGTAGTACAA
CAAGCCAGGATTGCCCAGAATGGAATTTTGGGAGACTTTATCATTAGATATGACGTCAATAG
AGAACAGAGCATTGGGGACATCCAGGTTCTAAATGGCTATTTTGTGCACTACTTTGCTCCTA
AAGACCTTCCTCCTTTACCCAAGAATGTGGTATTTCGTGCTTGACAGCAGTGCTTCTATGGTG
GGAACCAAACCTCCGGCAGACCAAGGATGCCCTCTTCACAATTCTCCATGACCTCCGACCCCA
GGACCGTTTCAGTATCATTGGATTTTCCAACCGGATCAAAGTATGGAAGGACCACTTGATAT
CAGTCACTCCAGACAGCATCAGGGATGGGAAAGTGACATTCACCATATGTCACCCACTGGA
GGCACAGACATCAACGGGGCCCTGCAGAGGGCCATCAGGCTCCTCAACAAGTACGTGGCCCA
CAGTGGCATTGGAGACCGGAGCGTGTCCCTCATCGTCTTCTGACGGATGGGAAGCCACGG
TCGGGGAGACGCACACCCTCAAGATCCTCAACAACACCCGAGAGGCGCGCCCGAGGCCAAGTC
TGCATCTTCACCATTTGGCATCGGCAACGACGTGGACTTCAGGCTGCTGGAGAACTGTGCT
GGAGAACTGTGGCCTCACACGCGCGTGCACGAGGAGGAGGACGCAGGCTCGCAGCTCATCG
GGTTCTACGATGAAATCAGGACCCCGCTCCTCTCTGACATCCGCATCGATTATCCCCCAGC
TCAGTGGTGCAGGCCACCAAGACCCTGTTCCCCAACTACTTCAACGGCTCGGAGATCATCAT
TGCGGGGAAGCTGGTGGACAGGAAGCTGGATCACCTGCACGTGGAGGTCACCGCCAGCAACA
GTAAGAAATTCATCATCCTGAAGACAGATGTGCCTGTGCGGCCTCAGAAGGCAGGGAAAGAT
GTCACAGGAAGCCCCAGGCCTGGAGGCGATGGAGAGGGGGACACCAACCACATCGAGCGTCT
CTGGAGCTACCTCACCACAAAGGAGCTGCTGAGCTCCTGGCTGCAAAGTGACGATGAACCGG
AGAAGGAGCGGCTGCGGCAGCGGGCCAGGCCCTGGCTGTGAGCTACCGCTTCCTCACTCCC
TTCACCTCATGAAGCTGAGGGGGCCGGTCCCACGCATGGATGGCCTGGAGGAGGCCACGG
CATGTCGGCTGCCATGGGACCCGAACCGGTGGTGCAGAGCGTGCAGAGGAGCTGGCACGCAGC
CAGGACCTTTGCTCAAGAAGCCAAACTCCGTCAAAAAAAAAAACAACAAAAACAAAAAAGA
CATGGGAGAGATGGTGTTTTTCTCTCCACCACCTGGGGATACGATTGAGAAAGATGGCCACCT
GCAAGCCAGGAAGACGGCCCTCACCAGACACCATGTCTGCTGGCACCTTGATCTTGACCTC
CCAGCCTCCAGAACTGTGAGAAATAAATGTGTTTTGTTTAAGCTAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 22

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192

<subunit 1 of 1, 694 aa, 1 stop

<MW: 77400, pI: 9.54, NX(S/T): 6

MLLLGLCLGLSLCVGSQEEAQSWGHSSEQDGLRVPRQVRLQLKTKPLMTEFSVKSTIIS
RYAFTTVSCRMLNRASEDQDIEFQMQUIPAAAFITNFTMLIGDKVYQGEITEREKKSGDRVKE
KRNKTTEENGEKGTETIFRASAVIPSKDKAAFFLSYEELLQRRLGKYEHSISVRPQQLSGRLS
VDVNILESAGIASLEVLPLHNSRQRGSGRGEDDSGPPPSTVINQNETFANIIFKPTVVQQAR
IAQNGILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVVFLDSSASMVGTK
LRQTKDALFTILHDLRPQDRFSIIIGFSNRIKVWKDHLISVTPDSIRDGKVYIHHMSPTGGTD
INGALQRAIRLLNKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKILNNTREAARGQVCIF
TIGIGNDVDVFRLLLEKLSLENCGLTRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVV
QATKTLFPNYFNGSEII IAGKLVDRLDHLHVEVTASNSKKFII LKTDVPVRPQKAGKDVTG
SPRPGGDGEGDTNHIERLWSYLTTKELLSSWLQSDDEPEKERLRQRAQALAVSYRFLTPFTS
MKLRGPVPRMDGLEEAHGMSAAMGPEPVVQSVRGAGTQPGPLLKKPNSVKKKQNKTKKRHGR
DGVFPLHHLGIR

Signal sequence.

amino acids 1-14

N-glycosylation sites.

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

Glycosaminoglycan attachment sites.

amino acids 213-217, 391-395

N-myristoylation sites.

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

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FIGURE 23

CGGACGCGTGGGGTGCCCCGACATGGCGAGTGTAGTGCTGCCGAGCGGATCCCAGTGTGCGGC
GGCAGCGGCGGGCGGCGGCCTCCCGGGCTCCGGCTTCTGCTGTTGCTCTTCTCCGCCGCGG
CACTGATCCCCACAGGTGATGGGCAGAATCTGTTTACGAAAGACGTGACAGTGATCGAGGGA
GAGGTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTTCAGCTACTGAA
TCCCAACAGGCAGACCATTTATTTTCAAGGACTTCAGGCCTTTGAAGGACAGCAGGTTTCAGT
TGCTGAATTTTTCTAGCAGTGAACCTCAAAGTATCATTGACAAACGTCTCAATTTCTGATGAA
GGAAGATACTTTTGCCAGCTCTATACCGATCCCCCACAGGAAAGTTACACCACCATCACAGT
CCTGGTCCCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGG
AGATTGAAGTCAACTGCACTGCTATGGCCAGCAAGCCAGCCACGACTATCAGGTGGTTCAAA
GGGAACACAGAGCTAAAAGGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGAC
CAGTCAGCTGATGCTGAAGGTGCACAAGGAGGACGATGGGGTCCCAGTGATCTGCCAGGTGG
AGCACCTGCGGTCACTGGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT
CAAGTGCACATTCAGATGACTTATCCTCTACAAGGCTTAACCCGGGAAGGGGACGCGCTTGA
GTTAACATGTGAAGCCATCGGGAAGCCCCAGCCTGTGATGGTAACCTTGGGTGAGAGTCGATG
ATGAAATGCCTCAACACGCCGTACTGTCTGGGCCCAACCTGTTTCATCAATAACCTAAACAAA
ACAGATAATGGTACATACCGCTGTGAAGCTTCAAACATAGTGGGGAAAGCTCACTCGGATTA
TATGCTGTATGTATACGATCCCCCACAACCTATCCCTCCTCCCACAACAACCACCACCACCA
CCACCACCACCACCACCACCATCCTTACCATCATCACAGATTCCCGAGCAGGTGAAGAAGGC
TCGATCAGGGCAGTGGATCATGCCGTGATCGGTGGCGTCGTGGCGGTGGTGGTGTTCGCCAT
GCTGTGCTTGCTCATCATTTCTGGGGCGCTATTTTGCCAGACATAAAGGTACATACTTCACTC
ATGAAGCCAAAGGAGCCGATGACGCAGCAGACGCAGACACAGCTATAATCAATGCAGAAGGA
GGACAGAACAACTCCGAAGAAAAGAAAGAGTACTTCATCTAGATCAGCCTTTTTTGTTCAT
GAGGTGTCCAACCTGGCCCTATTTAGATGATAAAGAGACAGTGATATTGG

FIGURE 24

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518

<subunit 1 of 1, 440 aa, 1 stop

<MW: 48240, pI: 4.93, NX(S/T): 7

MASVVLPSGSQCAAAAAAAAAAPPGLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISC
QVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSELKVSLTNVSISDEGRYFCQL
YTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKG
KSEVEEWSDMYTVTSQMLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMT
YPLQGLTREGDALELTCEAIGKPQPMVMTWVRVDDEMPQHAVLSGPNLFINNLNKTNDNGTYR
CEASNIVGKAHSDYMLYVYDPPTTIPPTTTTTTTTTTTTTTTTTILTIIITDSRAGEEGSIRAVDH
AVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEE
KKEYFI

Signal sequence.

amino acids 1-36

Transmembrane domain.

amino acids 372-393

N-glycosylation sites.

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,
430-434

Tyrosine kinase phosphorylation sites.

amino acids 233-240, 319-328

N-myristoylation sites.

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,
411-417, 427-433, 428-432

0943851.083001
T00E80" T58E4660

FIGURE 25

GGGGCGGGTGGACGCGGACTCGAACGCGAGTTGCTTCGGGACCCAGGACCCCCCTCGGGCCCCGA
CCCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCCGCCCCGGCTCCCTGCGCCGCCGCCGCCTC
CCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCT
GGGGCCTGGGGTGCAGGGCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCT
GCACTGCCCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTAC
GTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCTGCCGGGCCTGCA
GCTCCTGGACCTGTACAGAACAGATCGCCAGCCTGCGCCTGCCCCGCCTGCTGCTGCTGG
ACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGACACTGCCAACGTGGAG
GCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTCAGCCGCTTGCG
CAACCTCCACGACCTGGATGTGTCCGACAACAGCTGGAGCGAGTGCCACCTGTGATCCGAG
GCCTCCGGGGCCTGACGCGCCTGCGGCTGGCCGGCAACACCCGCATTGCCCAGCTGCGGGCC
GAGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGC
CCTGCCTGGCGACCTCTCGGGCCTCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCCGCAACC
CCTTCAACTGCGTGTGCCCCCTGAGCTGGTTTGGCCCCCTGGGTGCGCGAGAGCCACGTCA
CTGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCCGCCCAAGAACGCTGGCCGGCTGCTCCT
GGAGCTTGACTACGCCGACTTTGGCTGCCCAGCCACCACCACACAGCCACAGTGCCCA
CGAGGCCCCGTGGTGCGGGAGCCACAGCCTTGTCTTCTAGCTTGGCTCCTACCTGGCTTAGC
CCCACAGCGCCGCCACTGAGGCCCCAGCCCCGCCCTCCACTGCCCCACCGACTGTAGGGCC
TGTCCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGG
GGACACGGCACCACTGGCGTGCTTGTGCCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGC
CAGATGGGGCAGGGGACACGGCCCAGCCCTACACCAGTCACGCCGAGGGCCACCACGGTCCCT
GACCCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCC
AGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT
AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTGCG
GCCAACGCCACTTACTCCGTCTGTGTATGCCTTTGGGGCCCCGGGCGGGTGCCGGAGGGCG
AGGAGGCCTGCGGGGAGGCCCATACACCCCCAGCCGTCCACTCCAACCACGCCCCAGTCACC
CAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCCCGCCCTGGCCGCGGTGCTCCTGGC
CGCGCTGGCTGCGGTGGGGGCAGCCTACTGTGTGCGGCGGGGGCGGGCCATGGCAGCAGCGG
CTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGGCCCCTGGAACCTGGAGGGAGTGAAGGTC
CCCTTGGAGCCAGGCCCGAAGGCAACAGAGGGCGGTGGAGAGGGCCCTGCCCAGCGGGTCTGA
GTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCACCCCTCCACGCAAAGC
CCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGC
CAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGCAGA
CAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCATCTGTGAG
ATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCAGAACCGAGTGCCCTATGAGGACAGTGT
CCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCGGGGCCCTGCCATGTGCTGGTAAC
GCATGCCTGGGCCCTGCTGGGCTCTCCCACTCCAGGCGGACCCTGGGGGCCAGTGAAGGAAG
CTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGTGACTCTAGTCTTGGCCCCAGG
AAGCGAAGGAACAAAGAACTGGAAAGGAAGATGCTTTAGGAACATGTTTTTGTCTTTTAA
AATATATATATATTTATAAGAGATCCTTTCCCATTTATTCTGGGAAGATGTTTTTCAAACCTC
AGAGACAAGGACTTTGGTTTTTTGTAAGACAAACGATGATATGAAGGCCTTTTGTAAAGAAAA
ATAAAAAAAAAA

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804

<subunit 1 of 1, 598 aa, 1 stop

<MW: 63030, pI: 7.24, NX(S/T): 3

MCSRVP L L L L L L L L L L A L G P G V Q G C P S G C Q C S Q P Q T V F C T A R Q G T T V P R D V P P D T V G L Y V F E N
G I T M L D A S S F A G L P G L Q L L D L S Q N Q I A S L R L P R L L L L D L S H N S L L A L E P G I L D T A N V E A L R L
A G L G L Q Q L D E G L F S R L R N L H D L D V S D N Q L E R V P P V I R G L R G L T R L R L A G N T R I A Q L R P E D L A
G L A A L Q E L D V S N L S L Q A L P G D L S G L F P R L R L L A A A R N P F N C V C P L S W F G P W V R E S H V T L A S P
E E T R C H F P P K N A G R L L L E L D Y A D F G C P A T T T T A T V P T T R P V V R E P T A L S S S L A P T W L S P T A P
A T E A P S P P S T A P P T V G P V P Q P Q D C P P S T C L N G G T C H L G T R H H L A C L C P E G F T G L Y C E S Q M G Q
G T R P S P T P V T P R P P R S L T L G I E P V S P T S L R V G L Q R Y L Q G S S V Q L R S L R L T Y R N L S G P D K R L V
T L R L P A S L A E Y T V T Q L R P N A T Y S V C V M P L G P G R V P E G E E A C G E A H T P P A V H S N H A P V T Q A R E
G N L P L L I A P A L A A V L L A A L A A V G A A Y C V R R G R A M A A A A Q D K G Q V G P G A G P L E L E G V K V P L E P
G P K A T E G G G E A L P S G S E C E V P L M G F P G P G L Q S P L H A K P Y I

Signal sequence.

amino acids 1-23

Transmembrane domain.

amino acids 501-522

N-glycosylation sites.

amino acids 198-202, 425-429, 453-457

Tyrosine kinase phosphorylation site.

amino acids 262-270

N-myristoylation sites.

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

EGF-like domain cysteine pattern signature.

amino acids 355-367

Leucine zipper pattern.

amino acids 122-144, 194-216

FIGURE 27

GGCACTAGGACAACCTTCTTCCCTTCTGCACCACTGCCCCGTACCCTTACCCGCCCCGCCACC
TCCTTGCTACCCCACTCTTGAAACCACAGCTGTTGGCAGGGTCCCCAGCTCATGCCAGCCTC
ATCTCCTTTCTTGCTAGCCCCCAAAGGGCCTCCAGGCAACATGGGGGGCCCAGTCAGAGAGC
CGGCACTCTCAGTTGCCCTCTGGTTGAGTTGGGGGGCAGCTCTGGGGGCCGTGGCTTGTGCC
ATGGCTCTGCTGACCCAACAAACAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCA
GGGGACAGGAGGCCCCCTCCAGAATGGGGAAGGGTATCCCTGGCAGAGTCTCCCGGAGCAGA
GTTCCGATGCCCTGGAAGCCTGGGAGAATGGGGAGAGATCCCGGAAAAGGAGAGCAGTGCTC
ACCCAAAAACAGAAGAAGCAGCACTCTGTCCTGCACCTGGTTCCCATTAACGCCACCTCCAA
GGATGACTCCGATGTGACAGAGGTGATGTGGCAACCAGCTCTTAGGCGTGGGAGAGGCCTAC
AGGCCCAAGGATATGGTGTCCGAATCCAGGATGCTGGAGTTTATCTGCTGTATAGCCAGGTC
CTGTTTCAAGACGTGACTTTCACCATGGGTCAGGTGGTGTCTCGAGAAGGCCAAGGAAGGCA
GGAGACTCTATTCCGATGTATAAGAAGTATGCCCTCCCACCCGGACCGGGCCTACAACAGCT
GCTATAGCGCAGGTGTCTTCCATTTACACCAAGGGGATATTCTGAGTGTATAATTCCCCGG
GCAAGGGCGAAACTTAACCTCTCTCCACATGGAACCTTCCTGGGGTTTGTGAAACTGTGATT
GTGTTATAAAAAGTGGCTCCCAGCTTGGAAGACCAGGGTGGGTACATACTGGAGACAGCCAA
GAGCTGAGTATATAAAGGAGAGGGAATGTGCAGGAACAGAGGCATCTTCCTGGGTTTGGCTC
CCCGTTCCCTCACTTTTCCCTTTTCATTCCCACCCCCTAGACTTTGATTTTACGGATATCTTG
CTTCTGTTCCCCATGGAGCTCCG

094951.03004
FOREF-15864660

09-361-0830

MPASSPFL LAPKGPPGNMGGPVREPALSV ALWLSWGAALGAVACAMALLTQQTELQSLRREV
SRLQGTGGPSQNGEGYPWQSLPEQSSDALEAWENGERSRKRRAVLTQKQKKQH SVLHLVPIN
ATSKDDSDVTEVMWQPALRRGRGLQAQGYGVR IQDAGVYLLYSQVLFQDVTFTMGQVVSREG
OGROETLERCIRSMPSHPDRAYNSCY SAGVFHLHOGDILSVI IPRARAKNLNSPHGTFLGFVKL

amino acids 1-40

amino acids 124-128

amino acids 156-164

amino acids 36-42, 40-46, 179-185, 242-248

amino acids 34-45

FIGURE 29

CACTTTCTCCCTCTCTTCCTTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTCGCAGAGAC
 CTCGGAGACCGCGCCGGGAGACGGAGGTGCTGTGGGTGGGGGGACCTGTGGCTGCTCGTA
 CCGCCCCCACCCTCCTCTTCTGCACTGCCGTCTCCGGAAGACCTTTTCCCTGCTCTGTT
 TCCTTCACCGAGTCTGTGCATCGCCCCGGACCTGGCCGGGAGGAGGCTTGGCCGGCGGGAGA
 TGCTCTAGGGGCGGCGGGAGGAGCGGCCGGCGGGACGGAGGGCCCCGGCAGGAAGATGGGC
 TCCCGTGGACAGGGACTCTTGCTGGCGTACTGCCTGCTCCTTGCCTTTGCCTCTGGCCTGGT
 CCTGAGTCGTGTGCCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGC
 CGTCGCCTCCGGACCATGCCGAGAGGGCTGAAGAACAACATGAAAAATACAGGCCCAGTCAG
 GACCAGGGGCTCCCTGCTTCCCGGTGCTTGCCTGCTGTGACCCCGGTACCTCCATGTACCC
 GGCGACCGCCGTGCCCCAGATCAACATCACTATCTTGAAAGGGGAGAAGGGTGACCGCGGAG
 ATCGAGGCCTCCAAGGGAAATATGGCAAAACAGGCTCAGCAGGGGGCCAGGGGCCACACTGGA
 CCCAAAGGGCAGAAGGGCTCCATGGGGGCCCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGC
 CTTTTCGGTGGGCCCGGAAGAAGCCCATGCACAGCAACCACTACTACCAGACGGTGATCTTCG
 ACACGGAGTTCGTGAACCTCTACGACCACTTCAACATGTTACCGGCAAGTTCTACTGCTAC
 GTGCCCGGCCTCTACTTCTTCAGCCTCAACGTGCACACCTGGAACCAGAAGGAGACCTACCT
 GCACATCATGAAGAACGAGGAGGAGGTGGTGATCTTGTTTCGCGCAGGTGGGCGACCGCAGCA
 TCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTGGGTACGCCTC
 TACAAGGGCGAACGTGAGAACGCCATCTTCAGCGAGGAGCTGGACACCTACATCACCTTCAG
 TGGCTACCTGGTCAAGCACGCCACCGAGCCCTAGCTGGCCGGCCACCTCCTTTCTCTCGCC
 ACCTTCCACCCCTGCGCTGTGCTGACCCACCGCCTCTTCCCCGATCCCTGGACTCCGACTC
 CCTGGCTTTGGCATTCACTGAGACGCCCTGCACACACAGAAAGCCAAAGCGATCGGTGCTCC
 CAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAGGGCGGGGCACCCGC
 GAGAACCCTCTGGGACCTTCCGCGGCCCTCTCTGCACACATCCTCAAGTGACCCCGCACGGC
 GAGACGCGGGTGGCGGCAGGGCGTCCCAGGGTGCGGCACCGCGGCTCCAGTCCTTGGAATA
 ATTAGGCAAATTCTAAAGGTCTCAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAAGGG
 TTGTTATTTTGTCTTTCCAGCCAGCCTGCTGGCTCCCAAGAGAGAGGCCTTTTCAGTTGAG
 ACTCTGCTTAAGAGAAGATCCAAAGTTAAAGCTCTGGGGTCAAGGGAGGGGCCGGGGGCAGG
 AAACCTACCTCTGGCTTAATTCTTTTAAGCCACGTAGGAACCTTCTTGAGGGATAGGTGGACC
 CTGACATCCCTGTGGCCTTGCCCAAGGGCTCTGCTGGTCTTTCTGAGTCACAGCTGCGAGGT
 GATGGGGGCTGGGGCCCCAGGCGTCAGCCTCCCAGAGGGACAGCTGAGCCCCCTGCCTTGGC
 TCCAGGTTGGTAGAAGCAGCCGAAGGGCTCCTGACAGTGGCCAGGGACCCCTGGGTCCCCCA
 GGCCTGCAGATGTTTCTATGAGGGGCAGAGCTCCTTGGTACATCCATGTGTGGCTCTGCTCC
 ACCCTGTGCCACCCAGAGCCCTGGGGGGTGGTCTCCATGCCCTGCCACCCCTGGCATCGGCT
 TTCTGTGCCGCTCCACACAAATCAGCCCCAGAAGGCCCGGGGCTTGGCTTCTGTTTTT
 TATAAAACACCTCAAGCAGCACTGCAGTCTCCCATCTCCTCGTGGGCTAAGCATCACCGCTT
 CCACGTGTGTTGTGTTGGTTGGCAGCAAGGCTGATCCAGACCCCTTCTGCCCCACTGCCCT
 CATCCAGGCCTCTGACCAGTAGCCTGAGAGGGGCTTTTCTAGGCTTCAGAGCAGGGGAGAG
 CTGGAAGGGGCTAGAAAGCTCCCGCTTGTCTGTTTCTCAGGCTCCTGTGAGCCTCAGTCCTG
 AGACCAGAGTCAAGAGGAAGTACACGTCCCAATCACCCGTGTGAGGATTCACTCTCAGGAGC
 TGGGTGGCAGGAGAGGCAATAGCCCCCTGTGGCAATTGCAGGACCAGCTGGAGCAGGGTTGCG
 GTGTCTCCACGGTGCTCTCGCCCTGCCCATGGCCACCCAGACTCTGATCTCCAGGAACCC
 ATAGCCCCCTCTCCACCTCACCCCATGTTGATGCCAGGGTCACTCTTGCTACCCGCTGGGCC
 CCCAAACCCCCGCTGCCTCTCTTCCTTCCCCCATCCCCACCTGGTTTTGGACTAATCCTGC
 TTCCCTCTCTGGGCCTGGCTGCCGGGATCTGGGGTCCCTAAGTCCCTCTCTTTAAAGAACTT
 CTGCGGGTCACTCTGAAGCCGAGTTGCTGTGGGCGTGCCCGGAAGCAGAGCGCCACACTC
 GCTGCTTAAGCTCCCCCAGCTCTTTCCAGAAAACATTAAACTCAGAATTGTGTTTTCAA

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234

><subunit 1 of 1, 281 aa, 1 stop

><MW: 31743, pI: 6.83, NX(S/T): 1

MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEEQHEKYRP
SQDQGLPASRCLRCCDPGTSMYPATAVPQINITILKGEKGDRGDRGLQGKYGKTGSAGARGH
TGPKGQKGSMGAPGERCKSHYAAFSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMFTGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSQSLMLELREQDQVWV
RLYKGERENAIFSEELDTYITFSGYLVKHATEP

Signal sequence.

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

FOOEBO-TSBE4650

FIGURE 31

GCGGAGCATCCGCTGCGGTCTCTGCCGAGACCCCCGCGCGGATTTCGCCGGTCTTCCCCGCGG
GCGCGACAGAGCTGTCCTCGCACCTGGATGGCAGCAGGGGCGCCGGGGTCTCTCGACGCCA
GAGAGAAATCTCATCATCTGTGCAGCCTTCTTAAAGCAAATAAGACCAAGAGGGAGGATTAT
CCTTGACCTTTGAAGACCAAACTAACTGAAATTTAAAATGTTCTTTCGGGGGAGAAGGGAG
CTTGACTTACACTTTGGTAATAATTTGCTTCCTGACACTAAGGCTGTCTGCTAGTCAGAATT
GCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCTTTCTAAGGGAATC
AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTCTTGCTGTTCAAC
AAAAACATATCAGGGGACAAAGCATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTA
GACAACCCAACTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAGCA
AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
CCAAGAGTTACCCCAAGGAAGATTCTCTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCC
TAGCCCATCATCACACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCT
CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA
GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTTACAATTTTCTCTGATCAAGAAA
TAGCTCATCTGCTGCCTGAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCA
CATAACCTCGGCTACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACC
TTCTGGGACTTCCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC
AGCCTCCCACGACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG
GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA
AACCATAACGTTTACAGAAATCTCCAACCTTAACTTTGAACACAGGGAATGTGTATAACCCTA
CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCCTGGGAAGGT
AGGGAGGCCAGTCCAGGCAGTTCTCTCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCC
ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCCTGGTGATAGGCC
TCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTGGAT
TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGTCTCTTAATTCATT
TAGTAACCAGAAGCCCAAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTG
TATTTTGAAGACAGGAAAATGCCCCCTTCTGCTTTCCTTTTTTTTTTTGGAGACAGAGTCTT
GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAACCTCCGTCTC
CTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
CCACACCTGGGTGATTTTTGTATTTTTAGTAGAGACGGGGTTTCACCATGTTGGTCAGGCTG
GTCTCAAACTCCTGACCTAGTGATCCACCCTCCTCGGCCTCCCAAAGTGCTGGGATTACAGG
CATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTTTGGTTTTTGAGAAGGAATGAAGTG
GGAACCAAATTAGGTAATTTTGGGTAATCTGTCTCTAAAATATTAGCTAAAAACAAAGCTCT
ATGTAAAGTAATAAAGTATAATTGCCATATAAATTTCAAATTCAACTGGCTTTTATGCAAA
GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATTCTTGGTTCCAGATAAAATCAAC
TGTTTTATATCAATTTCTAATGGATTTGCTTTTCTTTTTATATGGATTTCCTTTAAACTTATT
CCAGATGTAGTTCCTTCCAATTAAATATTTGAATAAATCTTTTGTTACTCAA

094351-0300

FIGURE 32

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410

><subunit 1 of 1, 431 aa, 1 stop

><MW: 46810, pI: 6.45, NX(S/T): 6

MFFGGEGSLTYTLVIIICFLTLRLSASQNCLKKSLEDVVIDIQSSLKGIKRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHHTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTGNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFKWLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSLDYLINGIYVDI

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

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F00E90.T58E4660

FIGURE 33

GCGGCACCTGGAAGATGCGCCCATTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTC
GCCTCCTTGTGTGCCTGGTATTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT
GTCCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCCTCAAAGCTCCAGTCC
CCAAAAGGCAAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA
CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGG
AGAACAGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAAGTGGGA
ATGTGACAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAG
TTTATTCAGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCAC
AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACA
TGAAATTCAGGTCTAGCTGGGTATTTATTGCAGCAAAAGGCTTGGAAGTCCCTTCCGAAATT
CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACAACAGATATTCTGGCTGGCCTGCAGA
GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGCTTGACACTGCAGGGTCCTGAGTAAAT
GTGTTCTGTATAAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTTCTAAATCCAACA
GCCCATATTTGATGAGTATTTTGGGTTTGTGTAAACCAATGAACATTTGCTAGTTGTATCA
AATCTTGGTACGCAGTATTTTATACCAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGA
AACTAAAATGAATGGAAATTCTTAAAAAAAAA

09943851.083001

FIGURE 34

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777

><subunit 1 of 1, 235 aa, 1 stop

><MW: 25982, pI: 9.09, NX(S/T): 2

MRPLAGGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT
RCFDMYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPKERS

Signal sequence.

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125

094351 083004
T00E80" T58E4660